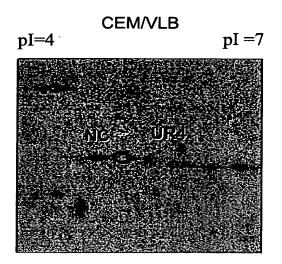


CEM pI=4 pI =7







Isoform 2 Results

ProF(	ProFound -Search Result Summary	n Result	Version 4.10.8 © 1997-2000 ProteoMetrics	7-2000	Versi Prote	Version 4.10.8 ProteoMetrics	0.8 ics
Prote	in Candidate	s for sea	Protein Candidates for search 20010608200436-0394208172123151 [73182 sequences searched]	ed]			
Rank	Rank Probability Est'd Z	Est'd Z	Protein Information and Sequence Analyse Tools (T)	% pl kDa ®	٩	kDa	⊗
<del>, -</del> +	1.0e+000 2.36	2.36	gi 5729877 ref NP_006588.1 Heat shock 70 kD protein 8, heat shock 70kD protein 8 (HSP73), heat shock cognate protein, 71 kDa,heat shock 70kd protein 10(HSC71) [Homo sapiens]	25 5.4 71.11 ®	5.4	71.11	R

### FIG. 2A

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Search Parameters
Details for rank 1 candidate in search 20010608200436-0394208172123151
gi 5729877 ref]NP_006588.1 heat shock 70 kD protein 8, heat shock 70kD protein 8 (HSP73), heat shock cognate
protein, 71 kDa,heat shock 70kd protein 10(HSC71) [Homo sapiens]
gi 13639862 ref XP_006086.2  heat shock 70kD protein 8 [Homo sapiens]
gi 123648 sp P11142 HS7C HUMAN HEAT SHOCK COGNATE 71 KDA PROTEIN
gi 87625 pir  1A27077 dnaK-type molecular chaperone-human
gi 32467 emb CAA68445.1 (Y00371)71 Kd heat shock cognate protein [Homo sapiens]
gi 13273304 gb AAK17898.1 AF352832_1(AF352832) constitutive heat shock protein 70 [Homo sapiens]
Sample ID NO CHANGE [Pass 0]
Measured peptides 20 20
Matched peptides 12 .
Min. sequence coverage 25%
FIG. 2B

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*25% of the amino acids of the HSC70 protein were represented in the amino acids of the mass peptides analyzed.
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12 Peptides	12 Peptides Measured Avg/ Computed	Avg/	Computed	Error	Error Residues Missed	ues M	lisse	p
Sequenced*	Mass (M) Mono	Mono	Mass	(wdd)	Start To		Cut	Cut Peptide sequence
•	1250.623	W	1250.611	10	237	246	0	MVNHFIAEFK
(								(1) +O@M;
-2-	1252.592	W	1252.608	-13	302	311	0	FEELNADLFR
	1406.696	Σ	1406.712	-12	237	247	Ţ	MVNHFIAEFKR
								(1) +0@M;
- 4	1479.743	W	1479.746	-2	300	311	1	ARFEELNADLFR
<b>.</b> ۲	1486.756	Σ	1486.693	42	37	49	0	TTPSYVAFTDTER
9 -	1690.705	X	1690.718	-٦	221	236	0	STAGDTHLGGEDFDNR
- 7	1786.968	Σ	1786.982	8	172	188	٦	IINEPTAAAIAYGLDKK
æ -	1820.874	Ψ	1820.883	-2	57	72	1	NQVAMNPTNTVFDAKR
								(1) +0@M;
<del>ဂ</del> ် -	1837.001	X	1837.005	-2	326	342	1	LDKSQIHDIVLVGGSTR
-10	1951.065	W	1951.052	7	452	469	~	DNNLLGKFELTGI PPAPR
	1980.996	W	1980.990	m	138	155	0	TVTNAVVTVPAYFNDSQR
-12	2773.258	W	2773.318	-21	424	447	0	QTQTFTTYSDNQPGVLIQVYEGER
- 1		.						

MSKGPAVGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA

**MNPTNTVFDAKR**LIGRRFDDAVVQSDMKHWPFMVVNDAGRPKVQVEYKGETKSFYPEEVS 61

121 SMVLTKMKEIAEAYLGKTVTNAVVTVPAYFNDSQRQATKDAGTIAGLNVLRIINEPTAAA

181 IAYGLDKKVGAERNVLIFDLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEDFDNRMVNH

241 FIAEFKRKHKKDISENKRAVRRLRTACERAKRTLSSSTQASIEIDSLYEGIDFYTSITRA

301 RFEELNADLFRGTLDPVEKALRDAKLDKSQIHDIVLVGGSTRIPKIQKLLQDFFNGKELN

421 PTKQTQTFTTYSDNQPGVLIQVYEGERAMTKDNNLLGKFELTGIPPAPRGVPQIEVTFDI 361 KSINPDEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPLSLGIETAGGVMTVLIKRNTTI

481 DANGILNVSAVDKSTGKENKITITNDKGRLSKEDIERMVQEAEKYKAEDEKQRDKVSSKN

541 SLESYAFNMKATVEDEKLQGKINDEDKQKILDKCNEIINWLDKNQTAEKEEFEHQQKELE

601 KVCNPIITKLYQSAGGMPGGMPGGFPGGGGAPPSGGASSGPTIEEVD

**BOLD** = Peptides covered by MS MALDI analysis

FIG. 3

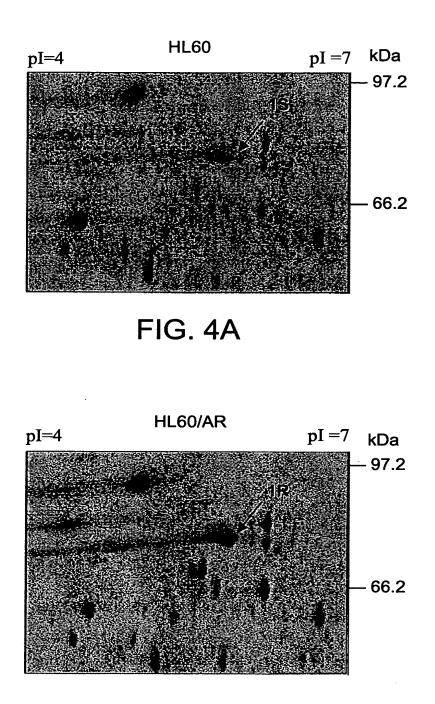


FIG. 4B

ProFc	ProFound -Search Result Summary	ı Result	Version 4.10.5 The Rockefeller University Edition	ر er Univ	/ersic versit	Version 4.10.5 iversity Edition	).5 on
Prote	Protein Candidates for search	s for se	rch BD36B5S9-CG5C-289FB336 [88967 sequences searched]				
Rank	Rank Probability Est'd Z	Est'd Z	Protein Information and Sequence Analyse Tools (T)	% pl kDa ®	þ	kDa	8
+	1.0e+000 2.43	2.43	T gi 5729877 ref NP_006588.1  (NM 006597) heat shock 70kd protein 8, heat shock 70kD protein 8(HSP73), heat shock cognate protein 71-kDa, heat shock 70kd protein 10 (HSC71) [Homo sapiens]	<u>26</u> 5.4 71.11 <sup>®</sup>	5.4	71.11	ø

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Search Parameters

Input Summary	r
Date & Time Mon Dec 17 01 01:33 2001 UTC (Search Time: 2 80 sec)	
Sample ID	
Database NCBInr (2001/12/11)	
Taxonomy Category Homo sapiens (human)	
Protein Mass Range 60 - 90 kDa	
Protein pl range 4.0 - 5.5	
Search for Single protein only	
Digest Chemistry Trypsin	
Max Missed Cut 2	
Modifications +C2H3ON@C(Complete), +O@M(Partial), &nbspC22H37N4O4S@K(Partial);	
Charge State MH+	
Peptide Masses (Da,Average)	
Tolerance(AVG) 100.00 ppm	
Peptide Masses 1199.667 1253.610 1401.805 1407.785 1463.128 1480.751 1487.698 1691.729   (Da,Monoisotopic) 1830.802 1838.043 1966.104 1982.001 1994.000 2231.141 2275.180 2278.081   2757.251 2774.246 2998.417 3548.224 3548.224	
Tolerance(MON) 100.00 ppm	
Number of Peptides 20	ЭЦ

7/28

5B

12 Peptides Sequenced\*

**QTQTFTTYSDNQPGVLIQVYEGER IVTNAVVTVPAYFNDSOR NSLESYAFNMKATVEDEK NQVAAMNPTNTVFDAKR** STAGDTHLGGEDFDNR -DKSQTHDIVLVGGSTR *NVQFAEKYKAEDEKQR* GTLDPVEKALRDAK **TPSYVAFTDTER** DAGTIAGLNVLR ARFEEINADLFR **MVNRFIAEFKR** FEELNADLFR Boxed peptides are biotinylated  $\circ \circ$ 0 0 2 0 0 0 49 236 342 155 533 22 171 311 247 325 311 447 557 138 518 160 302 237 300 37 326 312 424 540 221 57 -29 လု လု 46 9050 <u>3</u>0 10 -14 20 12 26% 1252.608 1980.956 2773.318 1198.666 1406.712 486.693 690.726 837.005 2274.136 479.746 1980.990 2997.452 965.083 Min. sequence coverage Measured peptides Matched peptides Σ Σ ΣΣ Σ ΣΣΣΖ ≥ ΣΣ ≥ 2773.238 2997.409 1252.602 965.096 1198.659 479.744 1486.690 837.035 1980.994 1980.994 2274.272 1406.777 690.721 γ Υ Υ Υ 4 5 9 7 8 ဝှ -10 -12 -13 1-

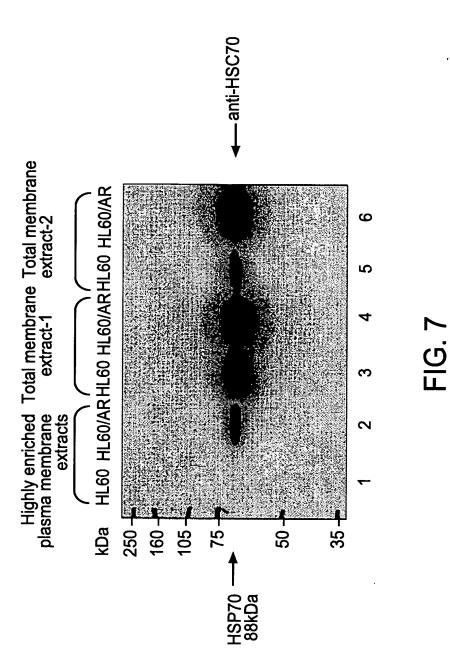
FIG. 5C

\*26% of the amino acids of the HSC70 protein were represented in the amino acids of the mass peptides analyzed. Note that 2 and 4 represent the same peptide

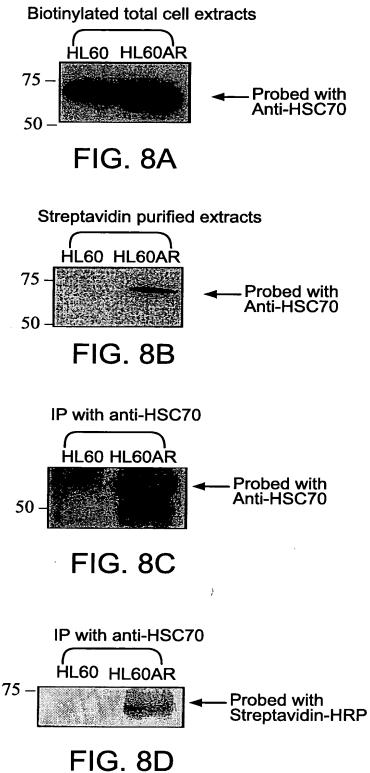
MSKGPAVGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAK<u>NQVA</u>

- **MNPTNTVFDAKR**LIGRRFDDAVVQSDMKHWPFMVVNDAGRPKVQVEYKGETKSFYPEEVS 61
- 121 SMVLTKMKEIAEAYLGKTVTNAVVTVPAYFNDSQRQATKDAGTIAGLNVLRIINEPTAAA
- 181 IAYGLDKKVGAERNVLIFDLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEDFDNRMVNH
- 241 FIAEFKRKHKKDISENKRAVRRLRTACERAKRTLSSSTQASIEIDSLYEGIDFYTSITRA
- 301 RFEELNADLFRGTLDPVEKALRDAKLDKSQIHDIVLVGGSTRIPKIQKLLQDFFNGKELN
  - 361 KSINPDEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPLSLGIETAGGVMTVLIKRNTTI
- 421 PTKQTQTFTTYSDNQPGVLIQVYEGERAMTKDNNLLGKFELTGIPPAPRGVPQIEVTFDI
- 481 DANGILNVSAVDKSTGKENKITITNDKGRLSKEDIER**MVQEAEKYKAEDEKQR**DKVSSK<u>N</u>
- 541 SLESYAFNMKATVEDEK CORRINDEDKOKILDKCNEIINWLDKNQTAEKEEFEHQQKELE
- 601 KVCNPIITKLYQSAGGMPGGMPGGFPGGGAPPSGGASSGPTIEEVD

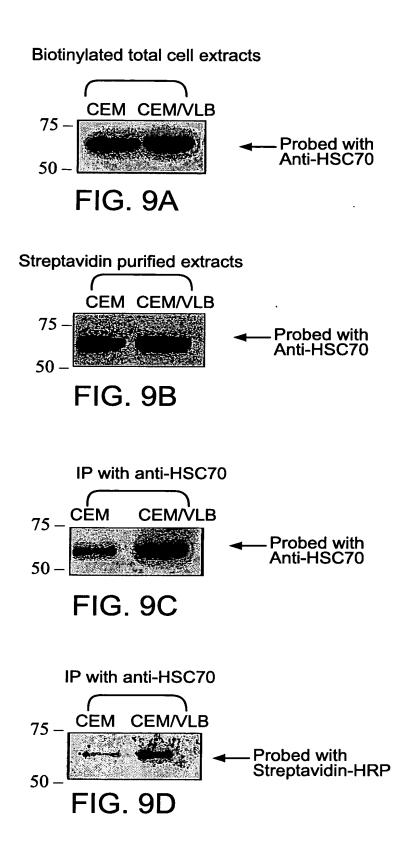
**BOLD** = Nonbiotinylated peptides specific for HSC70 Underlined & Italics = Biotinylated peptides

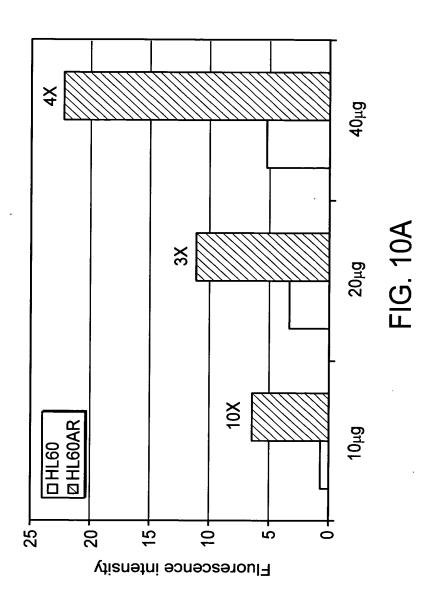






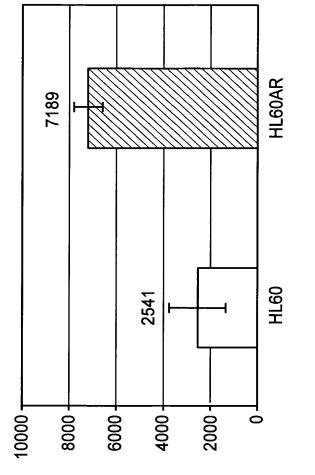


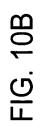




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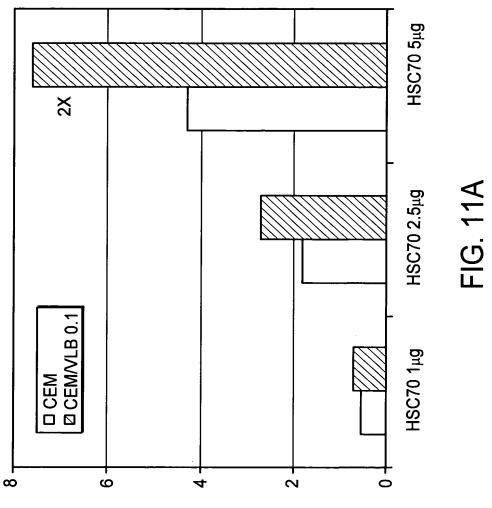




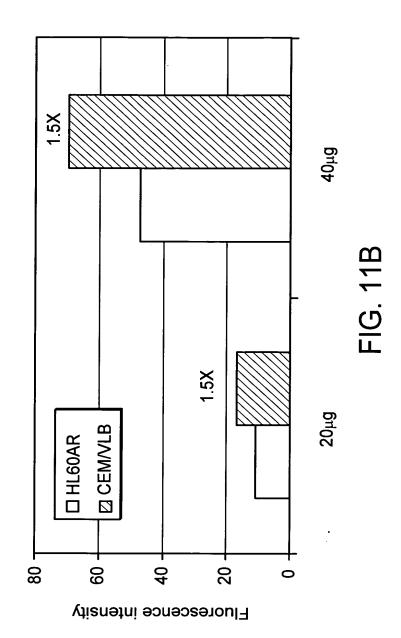


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Number of molecules per cell



Fluorescence Units



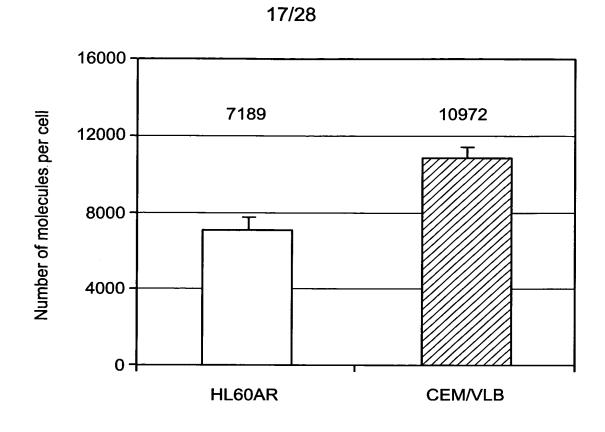


FIG. 11C

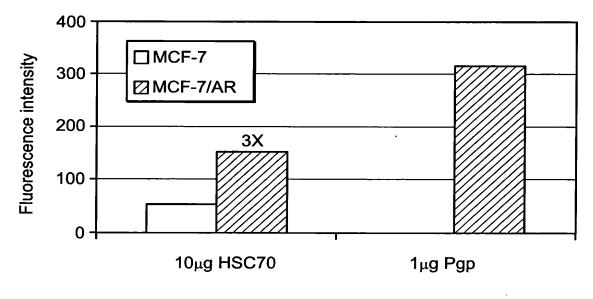


FIG. 12A

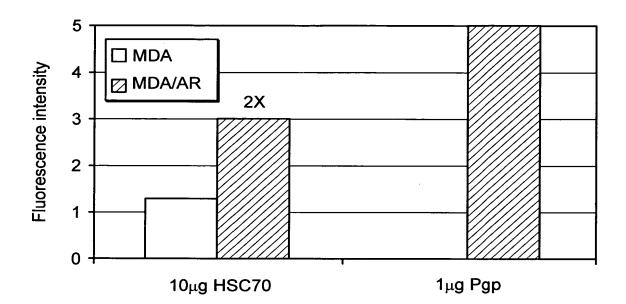
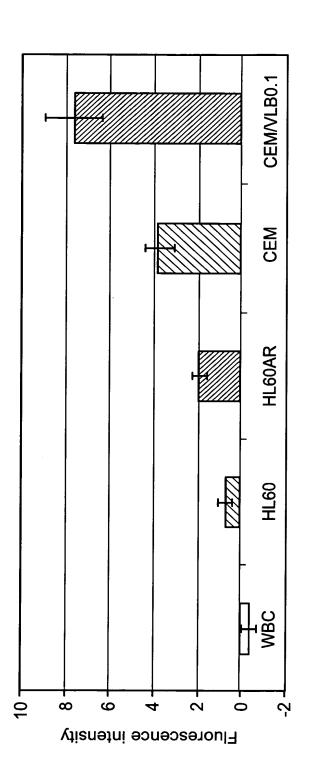
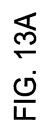


FIG. 12B



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# (GENBANK ACCESSION NO. AAK17898 (SEQ ID NO. 1)) POLYPEPTIDE SEOUENCE OF HUMAN HSC70

MSKGPAVGID LGTTYSCVGV FQHGKVEIIA NDQGNRTTPS YVAFTDTERL IGDAAKNQVA SMVLTKMKEI AEAYLGKTVT NAVVTVPAYF NDSQRQATKD AGTIAGLNVL RIINEPTAAA SLESYAFNMK ATVEDEKLQG KINDEDKQKI LDKCNEIINW LDKNQTAEKE EFEHQQKELE MNPTNTVFDA KRLIGRRFDD AVVQSDMKHW PFMVVNDAGR PKVQVEYKGE TKSFYPEEVS IAYGLDKKVG AERNVLIFDL GGGTFDVSIL TIEDGIFEVK STAGDTHLGG EDFDNRMVNH FIAEFKRKHK KDISENKRAV RRLRTACERA KRTLSSSTQA SIEIDSLYEG IDFYTSITRA RFEELNADLF RGTLDPVEKA LRDAKLDKSQ IHDIVLVGGS TRIPKIQKLL QDFFNGKELN KSINPDEAVA YGAAVQAAIL SGDKSENVQD LLLLDVTPLS LGIETAGGVM TVLIKRNTTI PTKQTQTFTT YSDNQPGVLI QVYEGERAMT KDNNLLGKFE LTGIPPAPRG VPQIEVTFDI DANGILNVSA VDKSTGKENK ITITNDKGRL SKEDIERMVQ EAEKYKAEDE KQRDKVSSKN TIEEVD KUCNPIITKL YQSAGGMPGG MPGGFPGGGA PPSGGASSGP 61 121 181 361 421 241 301 481 541 601

FIG. 14A

## FIG. 14B-1

1 ATGTCCAAGG GACCTGCAGT TGGTATTGAT CTTGGCACCA CCTACTCTTG TGTGGGTGTT 61 TTCCAGCACG GAAAGTCGA GATAATTGCC AATGATCAGG GAAACCGAAC CACTCCAAGC 121 TATGTCGCCT TTACGGACAC TGAACGGTTG ATCGGTGATG CCGCAAAGAA TCAAGTTGCA

(GENBANK ACCESSION NO. AF352832 (SEQ ID NO. 2)) **DNA SEQUENCE OF HUMAN HUMAN HSC70** 

FIG. 14B

<b>3. 14B-1</b>	3. 14B-2	Э. 14В-3	
FIG	FIG	FIG	

FIG. 14B-2

GCTGTTGTCC AGTCTGATAT GAAACATTGG CCCTTTATGG TGGTGAATGA TGCTGGCAGG TCTATGGTTC TGACAAAGAT GAAGGAAATT GCAGAAGCCT ACCTTGGGAA GACTGTTACC ATGAACCCCA CCAACACAGT TTTTGATGCC AAACGTCTGA TTGGACGCAG ATTTGATGAT CCCAAGGTCC AAGTAGAATA CAAGGGAGAG ACCAAAAGCT TCTATCCAGA GGAGGTGTCT CTTTGACCTG GGAGGTGGCA CTTTTGATGT GTCAATCCTC ACTATTGAGG ATGGAATCTT TGAGGTCAAG TCTACAGCTG GAGACACCCA CTTGGGTGGA GAAGATTTTG ACAACCGAAT GGTCAACCAT AGACGCCTCC GTACTGCTTG TGAACGTGCT AAGCGTACCC TCTCTTCCAG CACCCAGGCC AGTATTGAGA TCGATTCTCT CTATGAAGGA ATCGACTTCT ATACCTCCAT TACCCGTGCC CGATTTGAAG AACTGAATGC TGACCTGTTC CGTGGCACCC TGGACCCAGT AGAGAAAGCC CTTCGAGATG CCAAACTAGA CAAGTCACAG ATTCATGATA TTGTCCTGGT TGGTGGTTCT ACTCGTATCC CCAAGATTCA GAAGCTTCTC CAAGACTTCT TCAATGGAAA AGAACTGAAT AATGCTGTGG TCACAGTGCC AGCTTACTTT AATGACTCTC AGCGTCAGGC TACCAAAGAT GCTGGAACTA TTGCTGGTCT CAATGTACTT AGAATTATTA ATGAGCCAAC TGCTGCTGCT TTTATTGCTG AGTTTAAGCG CAAGCATAAG AAGGACATCA GTGAGAACAA GAGAGCTGTA ATTGCTTACG GCTTAGACAA AAAGGTTGGA GCAGAAGAA ACGTGCTCAT 181 301 241 361 421 481 541 901 961 1021 601 661 781 721 841

## FIG. 14B-3

1081 AAGAGCATCA ACCCTGATGA AGCTGTTGCT TATGGTGCAG CTGTCCAGGC AGCCATCTTG TCTGGAGACA AGTCTGAGAA TGTTCAAGAT TTGCTGCTCT TGGATGTCAC TCCTCTTTCC 1261 CCTACCAAGC AGACACAGAC CTTCACTACC TATTCTGACA ACCAGCCTGG TGTGCTTATT 1321 CAGGTTTATG AAGGCGAGCG TGCCATGACA AAGGATAACA ACCTGCTTGG CAAGTTTGAA CTCACAGGCA TACCTCCTGC ACCCCGAGGT GTTCCTCAGA TTGAAGTCAC TTTTGACATT GATGCCAATG GTATACTCAA TGTCTCTGCT GTGGACAAGA GTACGGGAAA AGAGAACAAG 1501 ATTACTATCA CTAATGACAA GGGCCGTTTG AGCAAGGAAG ACATTGAACG TATGGTCCAG GAAGCTGAGA AGTACAAAGC TGAAGATGAG AAGCAGAGGG ACAAGGTGTC ATCCAAGAAT AAGATTAACG ATGAGGACAA ACAGAAGATT CTGGACAAGT GTAATGAAAT TATCAACTGG 1741 CTTGATAAGA ATCAGACTGC TGAGAAGGAA GAATTTGAAC ATCAACAGAA AGAGCTGGAG CTTGGTATTG AAACTGCTGG TGGAGTCATG ACTGTCCTCA TCAAGCGTAA TACCACCATT 1621 TCACTTGAGT CCTATGCCTT CAACATGAAA GCAACTGTTG AAGATGAGAA ACTTCAAGGC 1801 AAGTTTGCA ACCCCATCAT CACCAAGCTG TACCAGAGTG CAGGAGGCAT GCCAGGAGGA 1861 ATGCCTGGGG GATTTCCTGG TGGTGGAGCT CCTCCCTCTG GTGGTGCTTC CTCAGGGCCC 1921 ACCATTGAAG AGGTTGATTA A 1201 1561 1141 1381 1441 1681

21	100
24	120

### Procedure for immunofluorescence (non-permeabilized cells)

2.5X10 <sup>4</sup> cells O/N in chamber slide in complete media
Block 30 min at RT with 100µl a-MEM/3%BSA/0.1%NaN <sub>3</sub>
Incubate with 1st antibody in 100 $\mu$ l a-MEM/3% BSA/0.1%NaN <sub>3</sub> for 1H at RT
Wash 6X with 200µl a-MEM/3% BSA.
Add 100µl of anti-mouse HRP (1:100) in a-MEM/3% BSA) for 30 min at RT
Wash 4X with 200µl a-MEM/3% BSA.
Add 50µl Tyramide 1:100 in Ampl. Buffer 0.0015% H <sub>2</sub> O <sub>2</sub> for 10 min at RT
Wash 4X with 200µl a-MEM/3% BSA.
Add 50µl streptavidin-FITC for 20min RT
Wash 4X with 200µl a-MEM/3% BSA.
Add 100µl (0.3µg) EMA in a-MEM, incubate 10 min. on ice under light
Wash 4X with 200µl a-MEM
Add 100µl of 4% paraformaldehyde in PBS for 20min at RT
Wash 4X with 200µl a-MEM

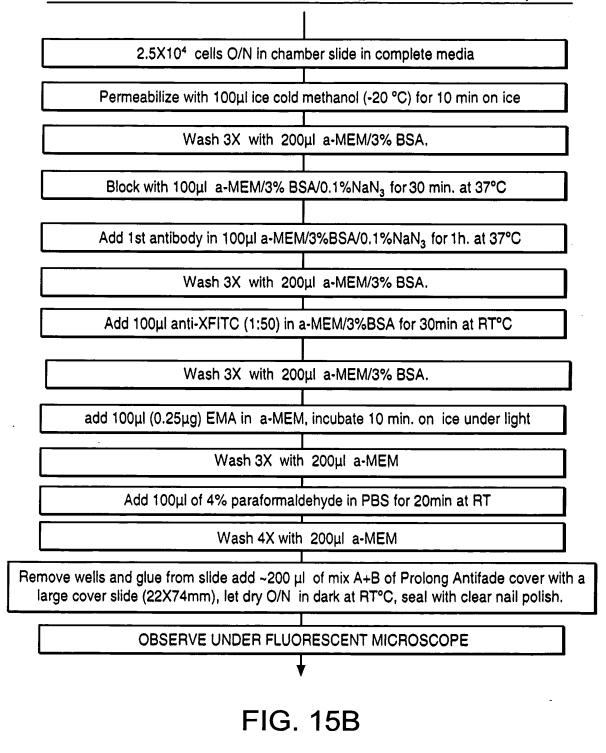
Remove wells and glue from slide add ~200 µl of mix A+B of Prolong Antifade cover with a large cover slide (22X74mm), let dry O/N in dark at RT°C, seal with clear nail polish.

### OBSERVE UNDER FLUORESCENT MICROSCOPE

FIG. 15A

Amplification kit used: TSA kit #2 with HRP-goat anti-mouse IgG and Alexa fluor 488 tyramide from molecular probes T-20192 ,

### Procedure for immunofluorescence (permeabilized cells)



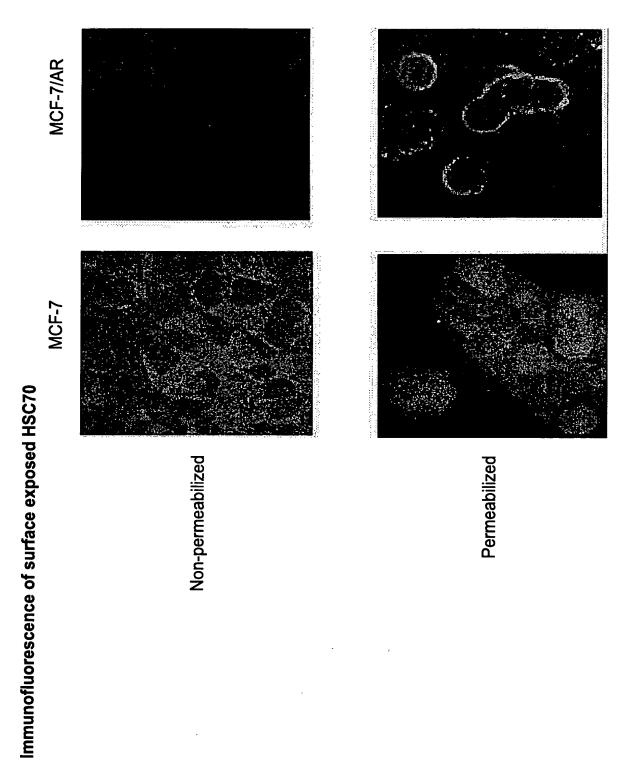
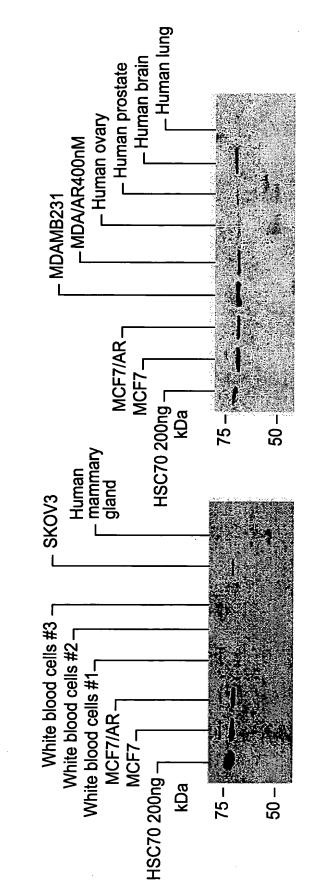


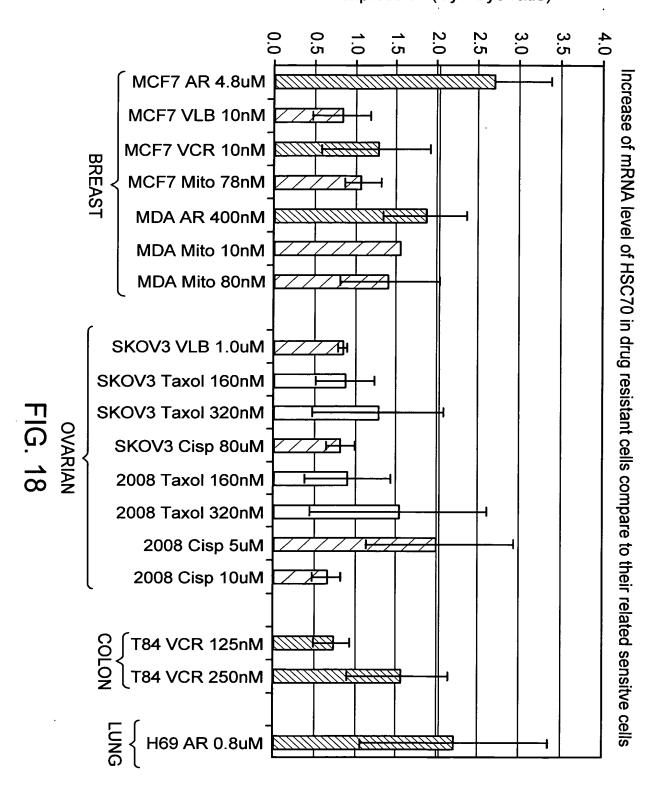
FIG. 16



HSC70 expression

FIG. 17

Fold increase in mRNA expression (Cy5/Cy3 ratio)



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